

FIGURE 1

GGGGGAGAAGGCGGCCGAGCCCCAGCTCTCCGAGCACCGGGTCGGAAGCCGCGACCCGAGCCGCGCAGGAA
GCTGGGACCGGAACCTCGGCGGACCCGGCCCCACCCAACCTCACCTGCGCAGGTACCCAGCACCCCTCGGAAC
CCAGAGGCCCCGCGCTCTGAAGGTGACCCCCCTGGGGAGGAAGGCGATGGCCCCCTGCGAGGACGATGGCCCC
CGCCCCGCTCGCCCCGGCCGGCATCCCTGCCGTGCGCTTGTGGCTTCTGTGCACGCTCGGCCCTCCAGGGCA
CCCAGGCCGGGCCACCGCCCGCCCCCTGGGCTGCCCCGCGGGAGCCGACTGCCTGAACAGCTTTACCGCC
GGGGTGCCTGGCTTCGTGCTGGACACCAACGCCTCGGTGAGCAACGGAGCTACCTTCTGGAGTCCCCCAC
CGTGCGCCGGGGCTGGGACTGCGTGCGCGCTGCTGCACCAACCCAGAACTGCAACTTGGCGCTAGTGGAGC
TGCAGCCCCGACCGCGGGGAGGACGCCATCGCCGCGCTGCTTCCTCATCAACTGCCTCTACGAGCAGAACTTC
GTGTGCAAGTTTCGCGCCCAGGGAGGGCTTCATCAACTACCTCACGAGGGAAGTGTACCGCTCCTACCGCCA
GCTGCGGACCCAGGGCTTTGGAGGGTCTGGGATCCCCAAGGCCTGGGCAGGCATAGACTTGAAGGTACAAC
CCCAGGAACCCCTGGTGCTGAAGGATGTGGAAAACACAGATTGGCGCCTACTGCGGGGTGACACGGATGTC
AGGGTAGAGAGGAAAGACCCAAACCAGGTGGAAGTGTGGGGACTCAAGGAAGGCACCTACCTGTTCCAGCT
GACAGTGAAGTACTGCTCAGACACCCAGAGGACACGGCCAACGTACAGTCACTGTGCTGTCCACCAAGCAGA
CAGAAGACTACTGCCTCGCATCCAACAAGGTGGGTGCGTGCCGGGGCTCTTTCCACGCTGGTACTATGAC
CCCACGGAGCAGATCTGCAAGAGTTTCGTTTTATGGAGGCTGCTTGGGCAACAAGAACAACCTACCTTCGGGA
AGAAGAGTGCATTCTAGCCTGTGGGGTGTGCAAGGTGGGCCTTTGAGAGGCAGCTCTGGGGCTCAGGCGA
CTTTCCCCCAGGGCCCCCTCCATGGAAAGGCGCCATCCAGTGTGCTCTGGCACCTGTGAGCCCAACCCAGTTC
CGCTGCAGCAATGGCTGCTGCATCGACAGTTTCCTGGAGTGTGACGACACCCCCAACTGCCCCGACGCCTC
CGACGAGGCTGCCTGTGAAAAATACACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGTGACA
AAGGGCACTGCGTGGACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTACAACCCC
TTCAGCGAACACTGCGCCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAACAACCTTTGAGGAAGAGCA
GCAGTGCCTCGAGTCTGTGCGGGCATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGGAAATCCCCATTC
CCAGCACAGGCTCTGTGGAGATGGCTGTGACAGTGTTCCTGGTCATCTGCATTGTGGTGGTGGTAGCCATC
TTGGGTTACTGCTTCTTCAAGAACCAGAGAAAGGACTTCCACGGACACCACCACCACCACCACCACCACC
TGCCAGCTCCACTGTCTCCACTACCGAGGACACGGAGCACCTGGTCTATAACCACACCACCCGGCCCCCTCT
GAGCCTGGGTCTCACCGGCTCTCACCTGGCCCTGCTTCCTGCTTGCCAAGGCAGAGGCCTGGGCTGGGAAA
AACTTTGGAACCAGACTCTTGCTGTTTCCCAGGCCCCACTGTGCTCAGAGACCAGGGCTCCAGCCCCCTCT
TGGAGAAGTCTCAGCTAAGCTCACGTCTGAGAAAGCTCAAAGGTTTGAAGGAGCAGAAAACCCCTGGGC
CAGAAGTACCAGACTAGATGGACCTGCCTGCATAGGAGTTTGGAGGAAGTTGGAGTTTTGTTTTCTCTGTT
CAAAGCTGCCTGTCCCTACCCCATGGTGCTAGGAAGAGGAGTGGGGTGGTGTGACACCCTGGAGGCCCCAA
CCCTGTCTCTCCGAGCTCCTCTTCCATGCTGTGCGCCCAGGGCTGGGAGGAAGGACTTCCCTGTGTAGTTT
GTGCTGTAAAGAGTTGCTTTTTGTTTATTTAATGCTGTGGCATGGGTGAAGAGGAGGGGAAGAGGCCTGTT
TGGCCTCTCTGTCTCTCTTCTTCCCCAAGATTGAGCTCTCTGCCCTTGATCAGCCCCACCCCTGGCC
TAGACCAGCAGACAGAGCCAGGAGAGGCTCAGCTGCATTCCGCAGCCCCCACCCTCAAGTTCTCCAACAT
CACAGCCCAGCCCACCCACTGGGTAATAAAAGTGGTTTGTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 2

MAPARTMARARLAPAGIPAVALWLLCTLGLQGTQAGPPPPAPPGLPAGADCLNSFTAGVPGFVLDTNASVSN
GATFLESPTVRRGWDCVRACCTTQNCNLALVELQPDREGDAIAACFLINCLYEQNFVCKFAPREGFINYL
REVYRSYRQLRTQGFGGSGIPKAWAGIDLKVQPQEPLVLKDVENTDWRLLRGDTDVRVERKDPNQVELWGL
KEGTYLFLQTLVTSSDHPEDTANVTVTVLSTKQTEDYCLASNKVGRCRGSFPRWYYDPTEQICKSFVYGGCL
GNKNNYLREEECILACRGVQGGPLRGSSGAQATFPQGSPMERRHPVCSGTCQPTQFRCSNGCCIDSFLECD
DTPNCPDASDEAAACEKYTSGFDELQRIHFPSDKGHCVDL PDTGLCKESI PRWYYPFSEHCARFTYGGCYG
NKNNFEEEQQCLESRCGISKKDVFGLRREIPI PSTGSVEMAVTVFLVICIVVVVAILGYCFFKNQRKDFHG
HHHHPPPTPASSTVSTTEDTEHLVYNHTRPL

signal sequence:	Amino acids 1-35
transmembrane domain:	Amino acids 466-483
N-glycosylation sites:	Amino acids 66-70;235-239;523-527.
N-myristoylation sites:	Amino acids 29-35;43-49;161-167; 212-218;281-287;282-288; 285-291;310-316;313-319; 422-428;423-429;426-432
Cell attachment sequence:	Amino acids 193-199
Pancreatic trypsin inhibitor (Kunitz) family signatures:	Amino acids 278-298;419-438

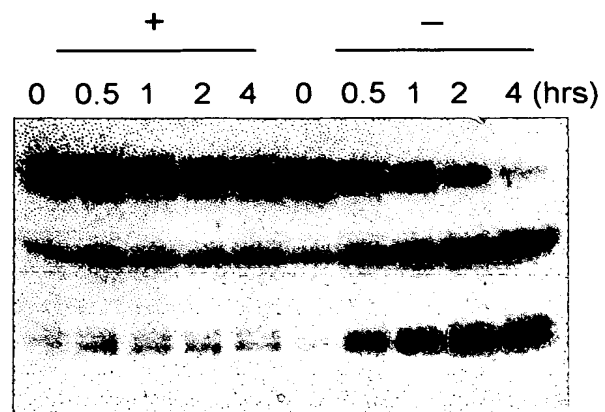


FIG. 3(a)

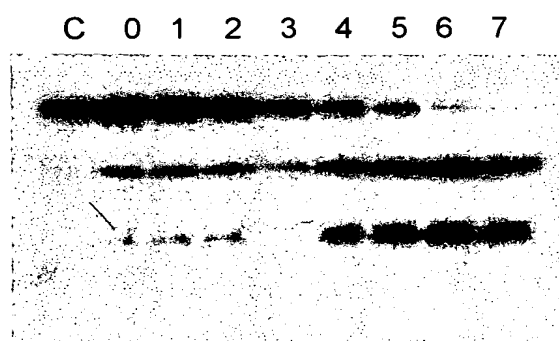


FIG. 3(b)

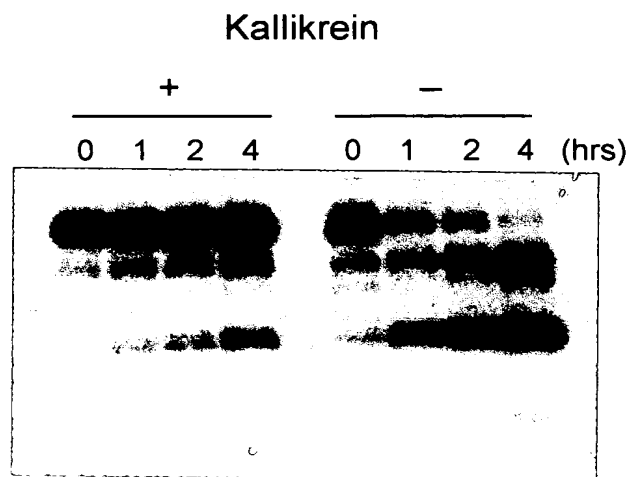


FIG. 4(a)

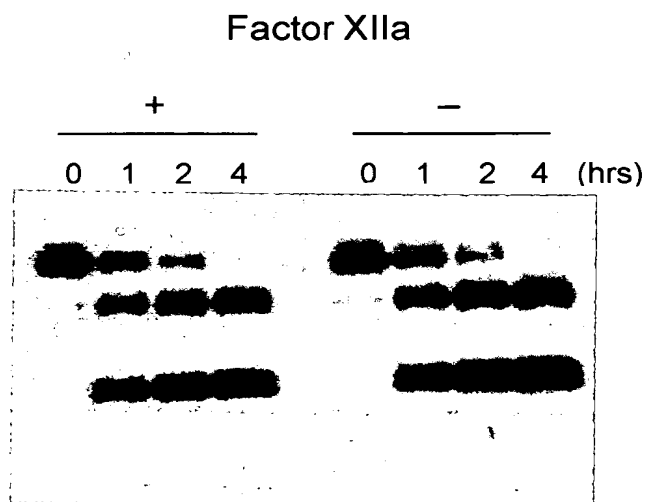


FIG. 4(b)

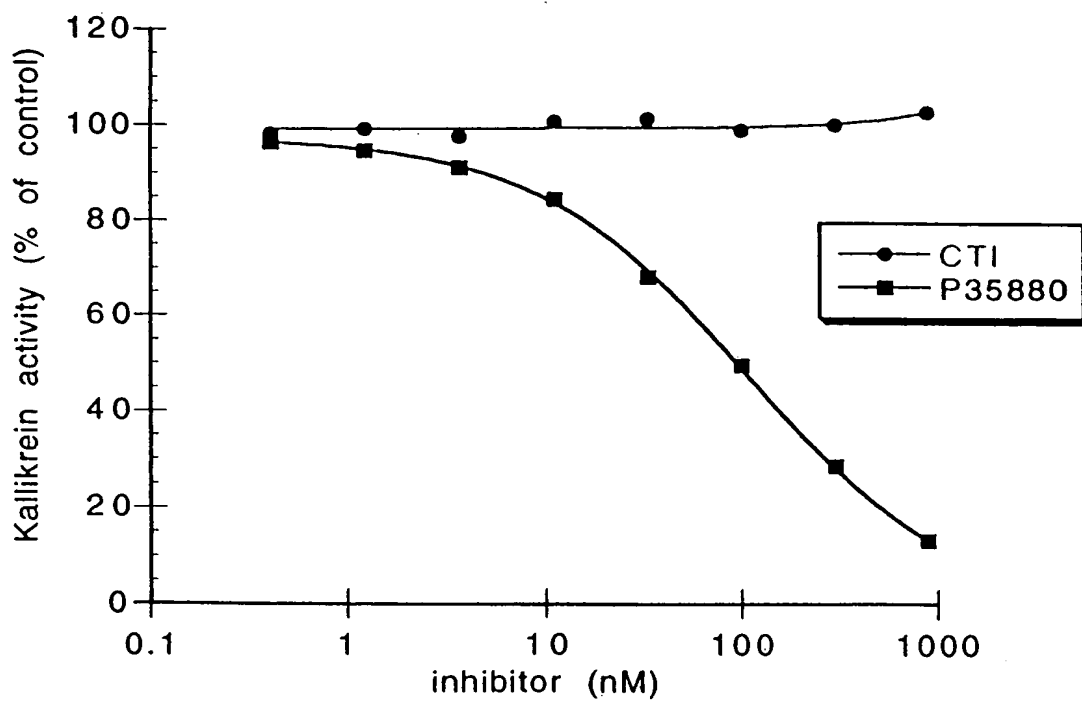


FIG. 5